

FIGURE 1

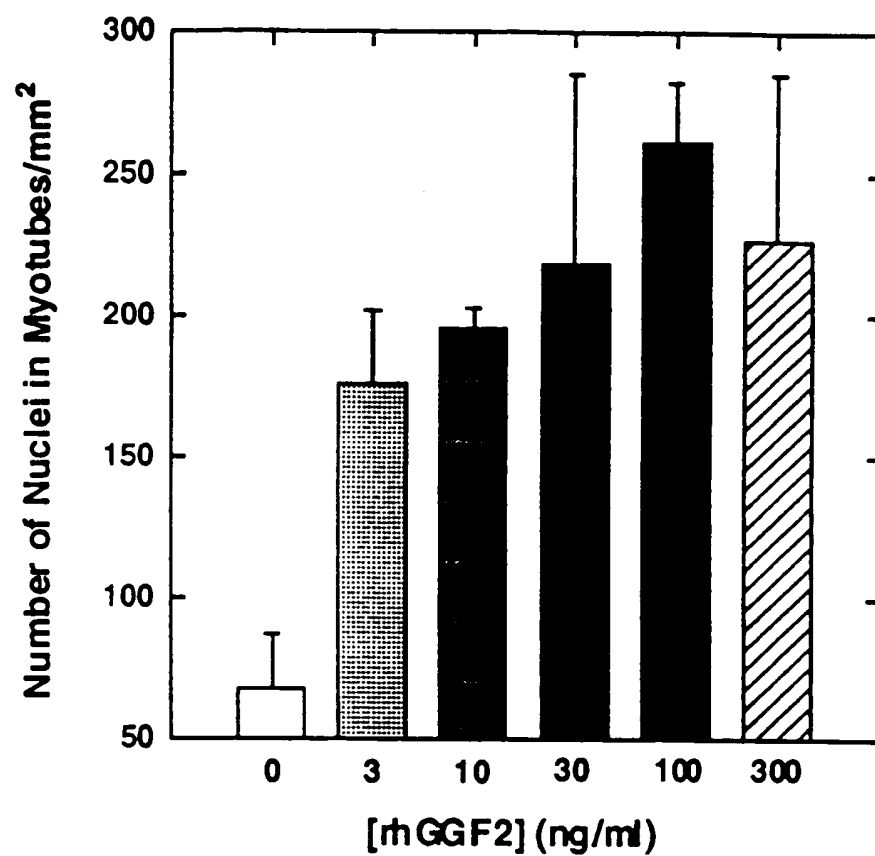


FIGURE 2

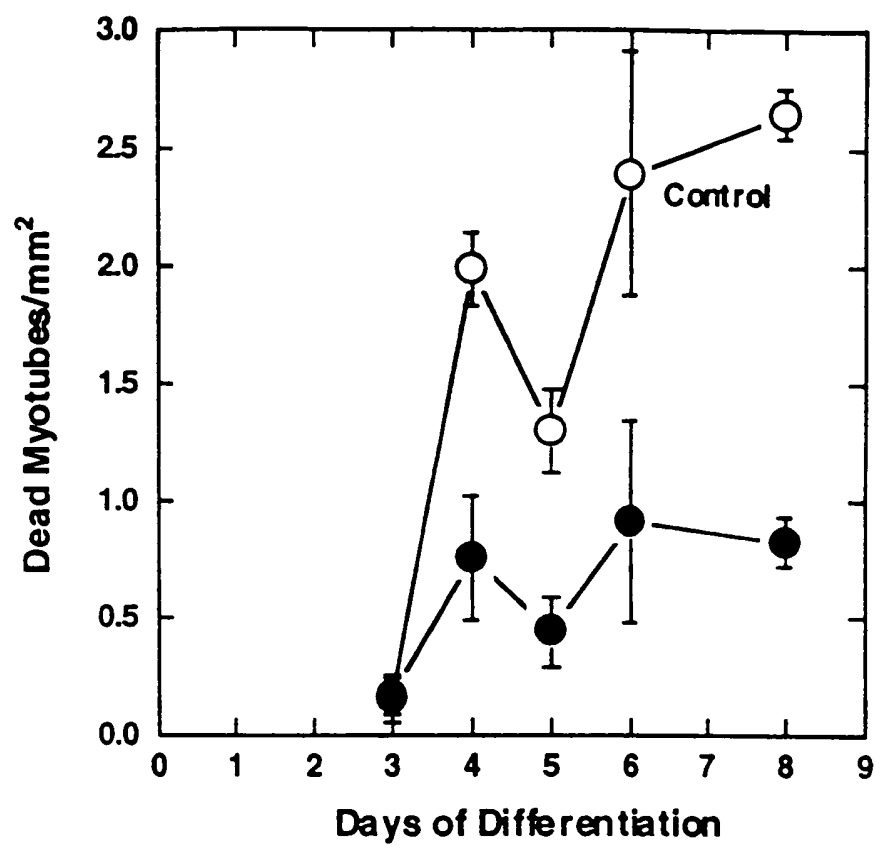


FIGURE 3

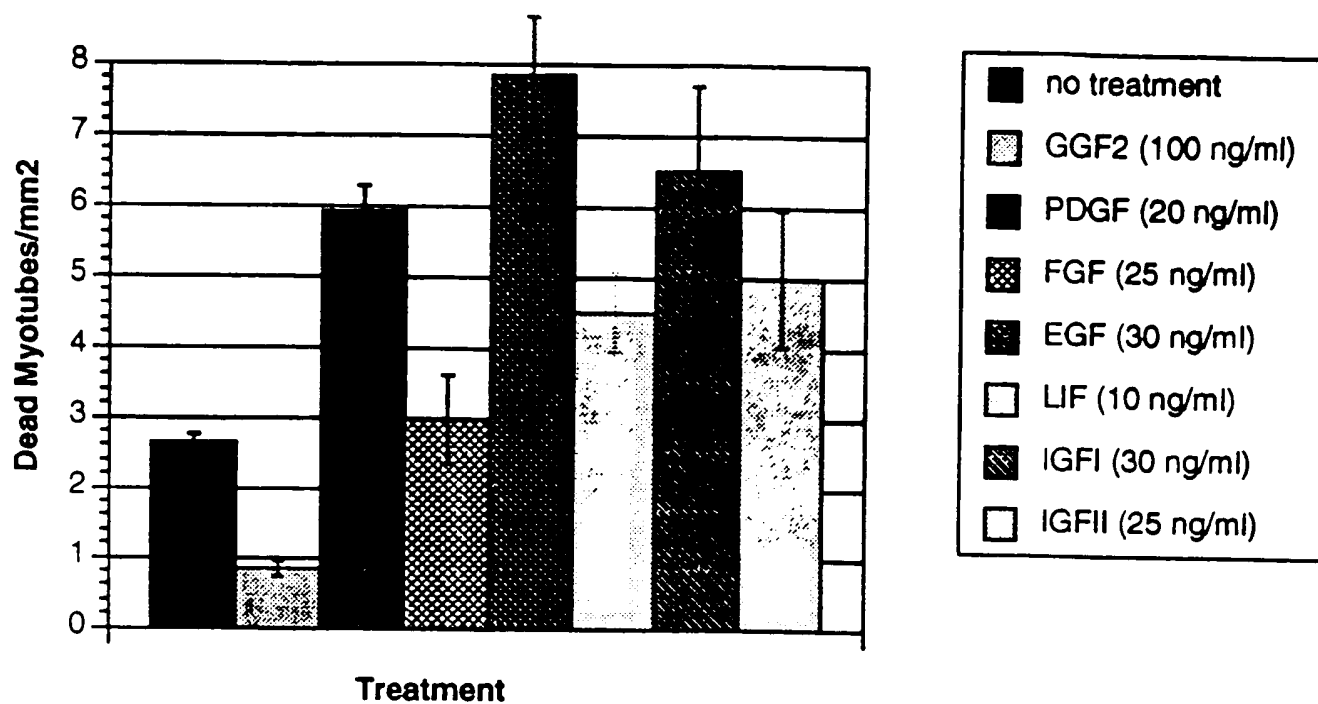


FIGURE 4

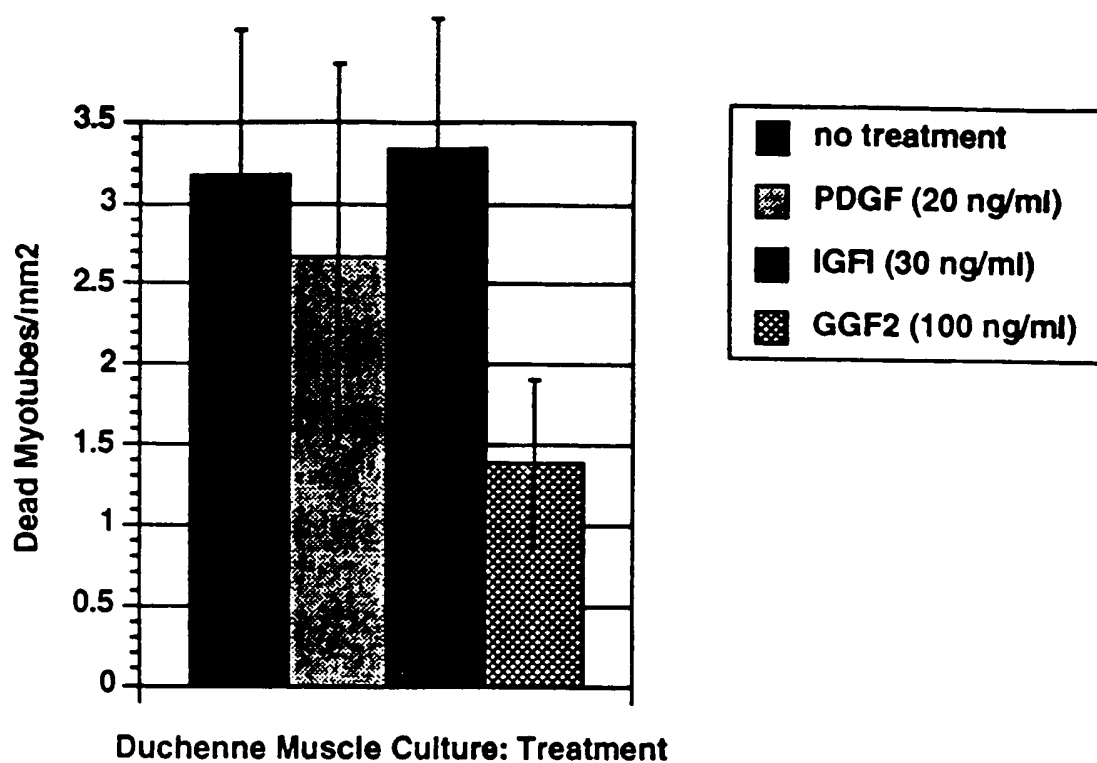


FIGURE 5

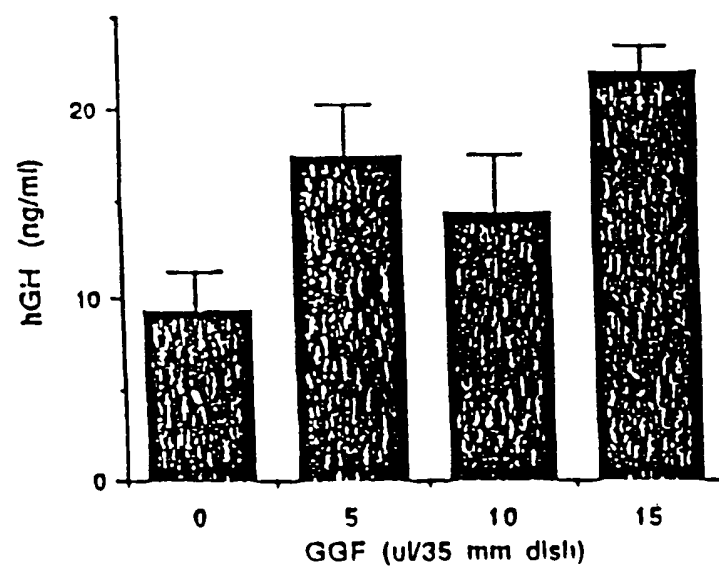


FIGURE 6

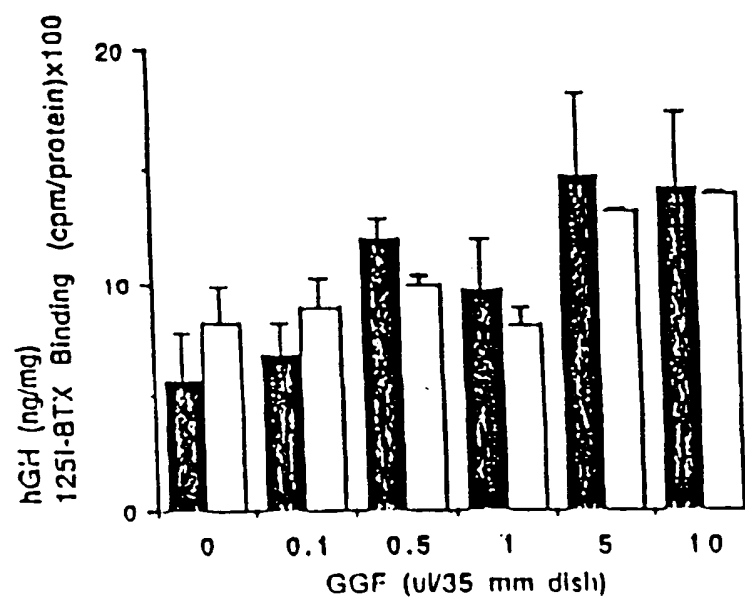


FIGURE 7

FIGURE 9

| | | | |
|---|----------|-----------------------|-----------------|
| A | OGF-1 01 | FKGDANTE | (SEQ ID NO: 1) |
| | OGF-1 02 | ASLADREYEMXK | (SEQ ID NO: 22) |
| | OGF-1 03 | TETSSSGLXLK | (SEQ ID NO: 23) |
| | OGF-1 07 | ASLADREYEMRK | (SEQ ID NO: 24) |
| | OGF-1 11 | AGYFAEXAR | (SEQ ID NO: 25) |
| | OGF-1 13 | TTEMASZOGA | (SEQ ID NO: 26) |
| | OGF-1 14 | AKZALALK | (SEQ ID NO: 27) |
| | OGF-1 15 | FVLOAKK | (SEQ ID NO: 28) |
| | OGF-1 17 | ETOPDPGOILKKVPNVIGAYT | (SEQ ID NO: 29) |
| | OGF-1 18 | EYKCLKPKWPKATVM | (SEQ ID NO: 17) |
| B | OGF-1 20 | EKKFYVP | (SEQ ID NO: 19) |
| | OGF-1 12 | KLEPLXAK | (SEQ ID NO: 32) |

FIGURE 10

| | | |
|-----------|--------------------------------|------------------|
| | Trypsin peptides | |
| GGF-II 01 | K/R VHQVWAAK* | (SEQ ID NO: 45) |
| GGF-II 02 | K/R YIFFMEPEAXSSG | (SEQ ID NO: 46) |
| GGF-II 03 | K/R LGAWGPPAFPVXY | (SEQ ID NO: 47) |
| GGF-II 04 | K/R WFVVIEGK* | (SEQ ID NO: 48) |
| GGF-II 05 | K/R ALAAAGYDVEK* | (SEQ ID NO: 164) |
| GGF-II 06 | K/R LVLK* | (SEQ ID NO: 165) |
| GGF-II 07 | K/R XXYPGQITSN | Histone H1 |
| GGF-II 08 | K/R ASPVSVGSVQELVQR* | |
| GGF-II 09 | K/R VCLLTVAALPPT | |
| GGF-II 10 | K/R DLLLXY | |
| | | Trypsin |
| | | (SEQ ID NO: 166) |
| | | (SEQ ID NO: 49) |
| | | (SEQ ID NO: 50) |
| | | (SEQ ID NO: 53) |
| | Lysyl Endopeptidase-C peptides | |
| GF-II 11 | KVHQVWAAK* | (SEQ ID NO: 51) |
| GF-II 12 | KASLADSGEYMXK* | (SEQ ID NO: 52) |

FIGURE 11

A

| | | |
|-----------|-----------------|-----------------|
| GGF-II 01 | VHQVWAAK | (SEQ ID NO: 45) |
| GGF-II 02 | YIFFMEPEAXSSG | (SEQ ID NO: 46) |
| GGF-II 03 | LGAWGPPAFPVXY | (SEQ ID NO: 47) |
| GGF-II 04 | WFVVIEGK | (SEQ ID NO: 48) |
| GGF-II 06 | ASPVSVGSVQELVQR | (SEQ ID NO: 49) |
| GGF-II 09 | VCLLTVAALPPT | (SEQ ID NO: 50) |
| GGF-II 11 | KVHQVWAAK | (SEQ ID NO: 51) |
| GGF-II 12 | KASLADSGEYMXK | (SEQ ID NO: 52) |

B

Novel Factor II Peptides - others

| | | |
|-----------|--------|-----------------|
| GGF-II 10 | DLLLXY | (SEQ ID NO: 53) |
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Comparison of BrUdR JSA and $[^{125}\text{I}]\text{UdR}$ autoradiography method for the DNA synthesis assay in Schwann cell cultures

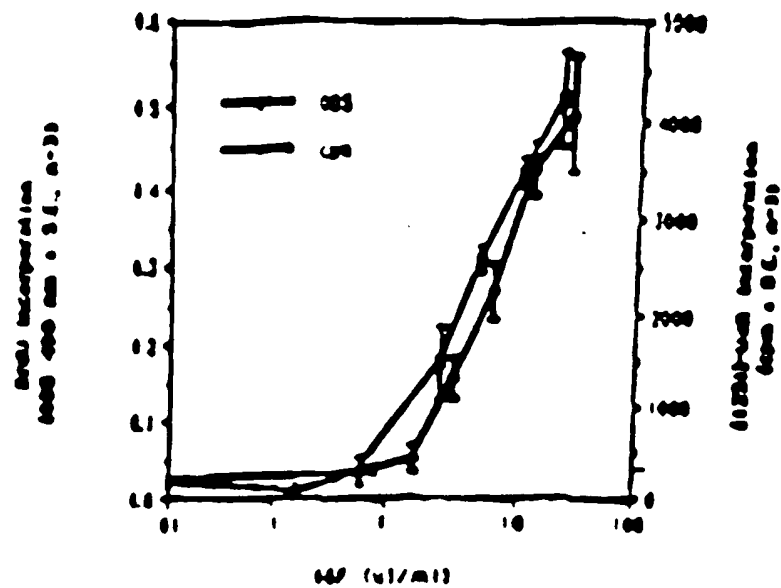


FIGURE 12

Comparison of Br-UdR immunoreactivity and Br-UdR labelled cell number

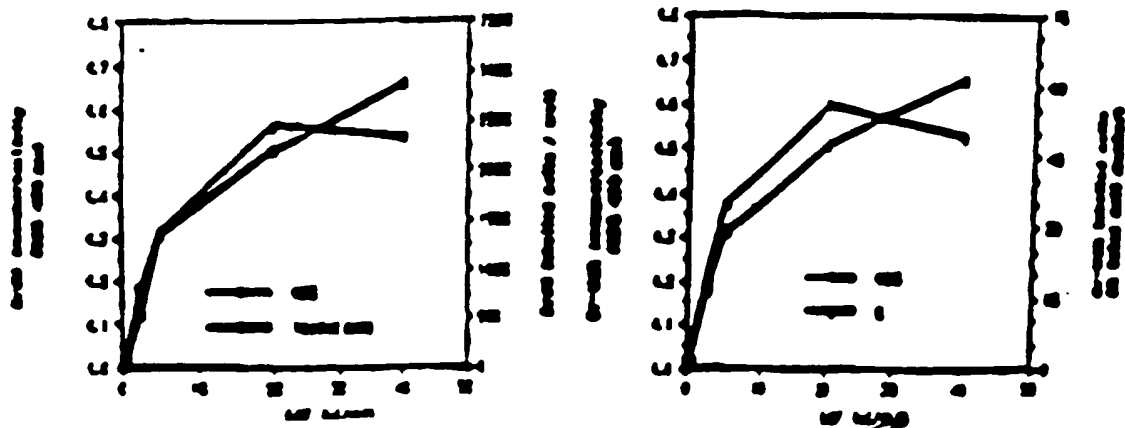


FIGURE 13A

FIGURE 13B

Mitogenic response of rat sciatic nerve Schwann cell to GGF₃

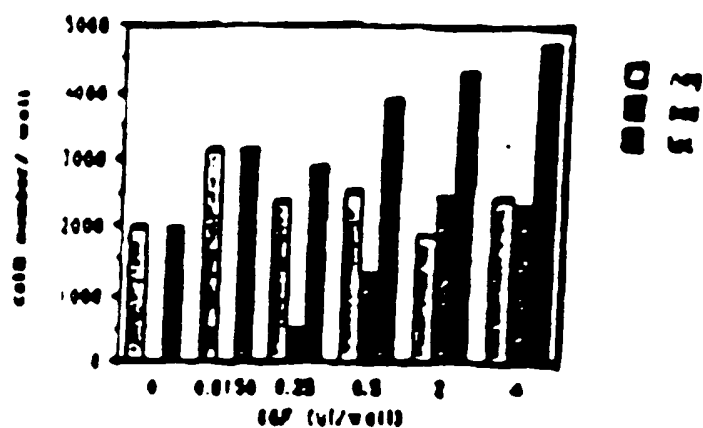


FIGURE 14

DNA synthesis in rat sciatic nerve Schwann cells and 3T3 fibroblasts in the presence of GGF₃

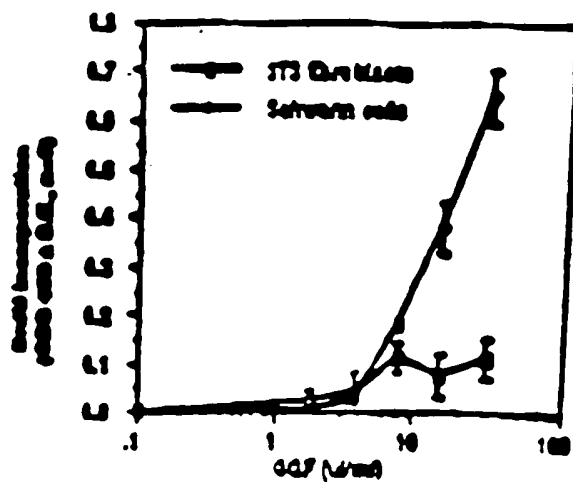


FIGURE 15

● Mitogenic response of BHK21 C13 cells
to FCS and GGFs

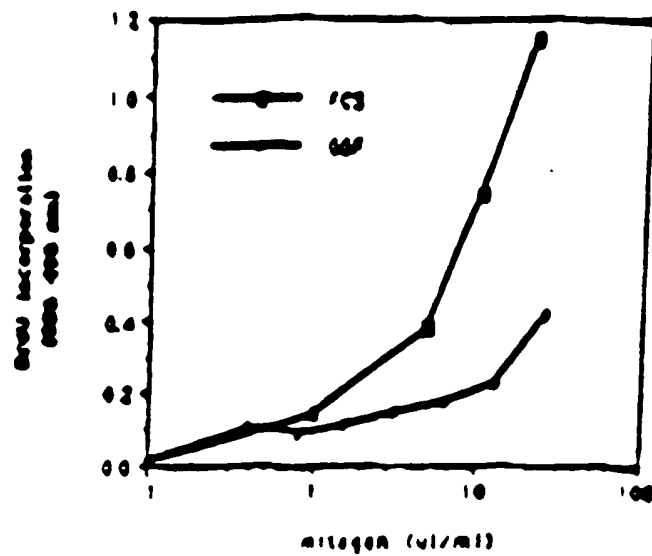


FIGURE 16

Survival and proliferation of BHK21 C13 cell
microcultures after 48 hours in presence of GGFs

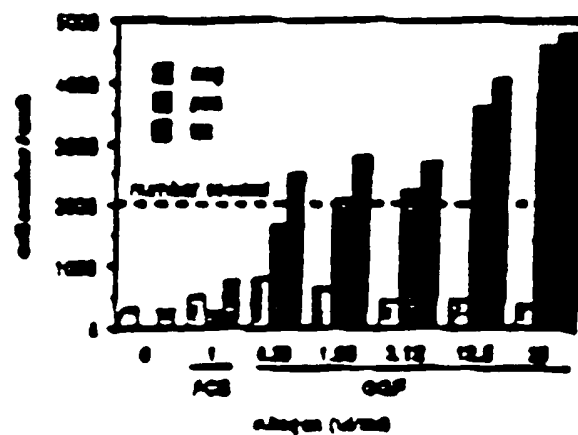


FIGURE 17

Mitogenic response of C6 cells to FCS

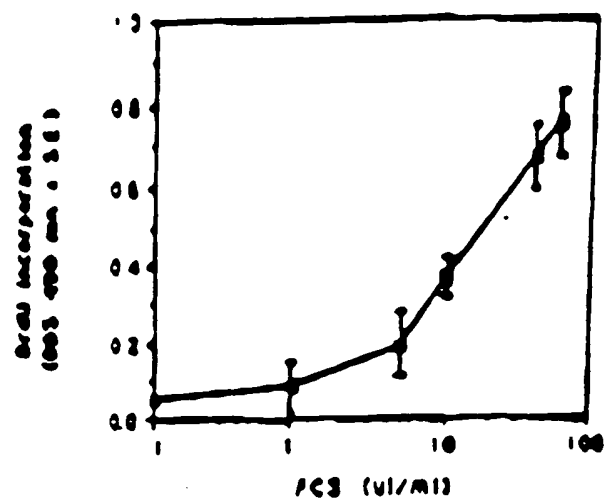


FIGURE 18

Mitogenic response of C6 cells to aFGF and GGFs

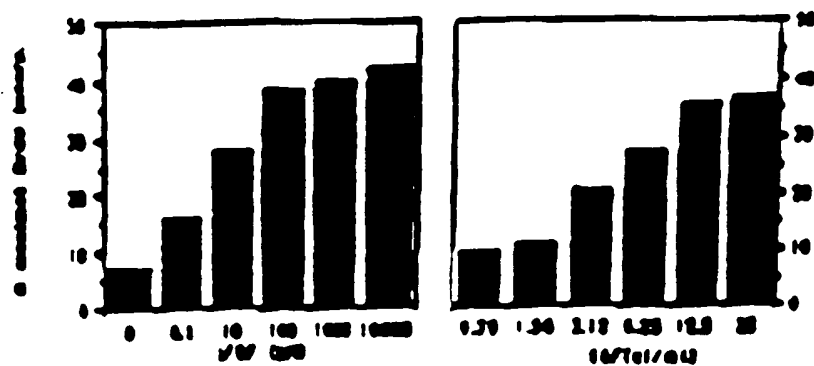


FIGURE 19

DEGRADATE OLIGONUCLEOTIDE PROBES FOR FACTOR I AND FACTOR II

| Oligo | Sequence | Peptide | |
|-------|------------------------|----------|-----------------|
| 535 | TTYAARGGNGAYGCNCAYAG! | GGPI-1 | (SEQ ID NO: 54) |
| 536 | CATRTAYTCRTAYTCRTONGC! | GGPI-2 | (SEQ ID NO: 55) |
| 537 | TGYTCNGANGCCATYTCNGT! | GGPI-13 | (SEQ ID NO: 56) |
| 538 | TGYTCNGTNGCCATYTCNGT! | GGPI-13 | (SEQ ID NO: 57) |
| 539 | CCDATNAGCATNGGNACTT! | GGPI-17 | (SEQ ID NO: 58) |
| 540 | GCHGCCAUACTGRTGAG! | GGPII-1 | (SEQ ID NO: 59) |
| 541 | GCYTCNGGYTCATRAAAG! | GGPII-2 | (SEQ ID NO: 60) |
| 542 | CCYTCDATNAGUAUACCA! | GGPII-4 | (SEQ ID NO: 61) |
| 543 | TCHGCCAUAATNGCHG! | GGPI-11 | (SEQ ID NO: 62) |
| 544 | GCHGCHAGNGCTTCYTTNGC! | GGPI-14 | (SEQ ID NO: 63) |
| 545 | GCHGCCAUAAGCTTCYTTNGC! | GGPI-14 | (SEQ ID NO: 64) |
| 546 | TTYTTNGCYTNGAGAACAA! | GGPI-15 | (SEQ ID NO: 65) |
| 551 | TTYTTNGCYTGYAUAACAA! | GGPI-15 | (SEQ ID NO: 66) |
| 568 | TGNAAGAGYTCYTGAG! | GGPII-6 | (SEQ ID NO: 67) |
| 569 | TGNAAGYAACTCYTGAG! | GGPII-6 | (SEQ ID NO: 68) |
| 609 | CATRTAYTCCHGUAATNGC! | GGPII-12 | (SEQ ID NO: 69) |
| 610 | CATRTAYTCCHGCTRTNGC! | GGPII-12 | (SEQ ID NO: 70) |
| 649 | NGARTCHGCTAUNGANGCTT! | GGPII-12 | (SEQ ID NO: 71) |
| 650 | NGARTCHGCUAGNGANGCTT! | GGPII-12 | (SEQ ID NO: 72) |
| 651 | RCTRTCHGCTAUNGANGCTT! | GGPII-12 | (SEQ ID NO: 73) |
| 652 | RCTRTCHGCUAGNGANGCTT! | GGPII-12 | (SEQ ID NO: 74) |
| 653 | NGARTCHGCTAAGCTNGCTT! | GGPII-12 | (SEQ ID NO: 75) |
| 654 | NGARTCHGCHAGCTNGCTT! | GGPII-12 | (SEQ ID NO: 76) |
| 655 | RCTRTCHGCTAAGCTNGCTT! | GGPII-12 | (SEQ ID NO: 77) |
| 656 | RCTRTCHGCUAGCTNGCTT! | GGPII-12 | (SEQ ID NO: 78) |
| 659 | ACHAGAGAAAGGCTGAG! | GGPI-13 | (SEQ ID NO: 79) |
| 660 | ACHAGAGAAAGGCTGAG! | GGPI-13 | (SEQ ID NO: 80) |
| 661 | CAYCAAGTATGGGCHGGA! | GGPII-1 | (SEQ ID NO: 81) |
| 662 | TTYGTNGTATGAGGGA! | GGPII-4 | (SEQ ID NO: 82) |
| 663 | AARGCHAYGCNCAYAGGA! | GGPI-1 | (SEQ ID NO: 83) |
| 664 | CARGCTTNGCHGCTTGA! | GGPI-14 | (SEQ ID NO: 84) |
| 665 | GTNGCTTNGCTCAGAGTT! | GGPII-6 | (SEQ ID NO: 85) |
| 666 | GTNGCTTNGCTCAGAGTT! | GGPII-6 | (SEQ ID NO: 86) |
| 694 | NAGTTTTTGAAGATTCGCC! | GGPI-17 | (SEQ ID NO: 87) |

FIGURE 20

ANALYSIS OF THE DATA FROM THE SURVEY

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Degenerate PCR primers

| Oligo | Sequence | Peptide | |
|-------|--|----------|------------------|
| 657 | CCGAATTCTGCAGGARAACACACGAYCCGCG! | GGPII-17 | (SEQ ID NO: 90) |
| 658 | AAGGATCTCTGCAGNGTRTANGONCCATNACCATNGG! | GGPII-17 | (SEQ ID NO: 91) |
| 667 | CCGAATTCTGCAGGONGAYTCGNGGARTAYATG! | GGPII-12 | (SEQ ID NO: 92) |
| 668 | CCGAATTCTGCAGGONGAYATTCGNGGARTAYAT! | GGPII-12 | (SEQ ID NO: 93) |
| 669 | AAGGATCTCTGCAGNNHCATRTAYTCHCNGARTC! | GGPII-12 | (SEQ ID NO: 94) |
| 670 | AAGGATCTCTGCAGNNHCATRTAYTCHCCTRTCTC! | GGPII-12 | (SEQ ID NO: 95) |
| 671 | CCGAATTCTGCAGCAYCAROTNTGGGNGGCHAA! | GGPII-1 | (SEQ ID NO: 96) |
| 672 | CCGAATTCTGCAGATHTTYYTYYATGCAACGARG! | GGPII-2 | (SEQ ID NO: 97) |
| 673 | CCGAATTCTGCAGGGGCGNCGNCGNCHTTTCNGT! | GGPII-3 | (SEQ ID NO: 98) |
| 674 | CCGAATTCTGCAGTGGTTTGTNTYATGCAAGG! | GGPII-4 | (SEQ ID NO: 99) |
| 677 | AAGGATCTCTGCAGYTTNGCGGCCAAYCTGRTG! | GGPII-1 | (SEQ ID NO: 100) |
| 678 | AAGGATCTCTGCAGGCTTCNGGYTCAATRAAAR! | GGPII-2 | (SEQ ID NO: 101) |
| 679 | AAGGATCTCTGCAGACNGGRAUNGCHGNGGNGCC! | GGPII-3 | (SEQ ID NO: 102) |
| 680 | AAGGATCTCTGCAGYTTNCCYTCATNACNACRAAC! | GGPII-4 | (SEQ ID NO: 103) |
| 681 | CATRTAYTCTRTAYTCTCHGCAAGGATCTCTGCAG! | GGPII-2 | (SEQ ID NO: 104) |
| 682 | CCGAATTCTGCAGAAAGGNGAYGCHAYACHCA! | GGPII-1 | (SEQ ID NO: 105) |
| 683 | CGNGCYAANGCYRCYTTNGCAAGGATCTCTGCAG! | GGPII-14 | (SEQ ID NO: 106) |
| 684 | CGNGCHAGNGCYTCYTTNGCAAGGATCTCTGCAG! | GGPII-14 | (SEQ ID NO: 107) |
| 685 | TCHGCAARTANCGCHGCAAGGATCTCTGCAG! | GGPII-1 | (SEQ ID NO: 108) |

Unique PCR primers for Factor II

| Oligo | Sequence | Comment | |
|-------|---|-------------------|------------------|
| 711 | CATCGATCTGCAGGCTGATCTCGAGAATATATGTGCA! | 3' RACE | (SEQ ID NO: 109) |
| 712 | AAGGATCTCTGCAGCCACATCTCGAGTCGACATCGATT! | 3' RACE | (SEQ ID NO: 110) |
| 713 | CCGAATTCTGCAGTGAATCAGCAACTACGAAATGACA! | 3' RACE | (SEQ ID NO: 111) |
| 721 | CATCGATCTGCAGGCTAGTTTGCTGATCACTTTGCAG! | 5' RACE | (SEQ ID NO: 112) |
| 722 | AAGGATCTCTGCAGTAAATTTCTCGAAATCAGCCAGTG! | 5' RACE; ANCHORED | (SEQ ID NO: 113) |
| 725 | AAGGATCTCTGCAGGCAAGCAATAGGCAATCTCTTA! | EXON A | (SEQ ID NO: 114) |
| 726 | CCGAATTCTGCAGCAGAACTTGCATTAGCAAAAG! | EXON A | (SEQ ID NO: 115) |
| 771 | CATCCCCGATGAAGATCAGAGTCTGTGGCA! | EXONS 3+4 | (SEQ ID NO: 116) |
| 772 | ATACCCCGGCTGCAGAACATGAGATTTCACACCTGCG! | EXONS 3+4 | (SEQ ID NO: 117) |
| 773 | AAGGATCTCTCAATTTGCAACTGCCACAGACTCTT! | ANCHORED | (SEQ ID NO: 118) |
| 776 | ATACCCCGGCTGCAGATGAGATTTCACACCTGCGTGA! | EXONS 3+4 | (SEQ ID NO: 119) |

Summary of contiguous GGF-II cDNA structures and sequences

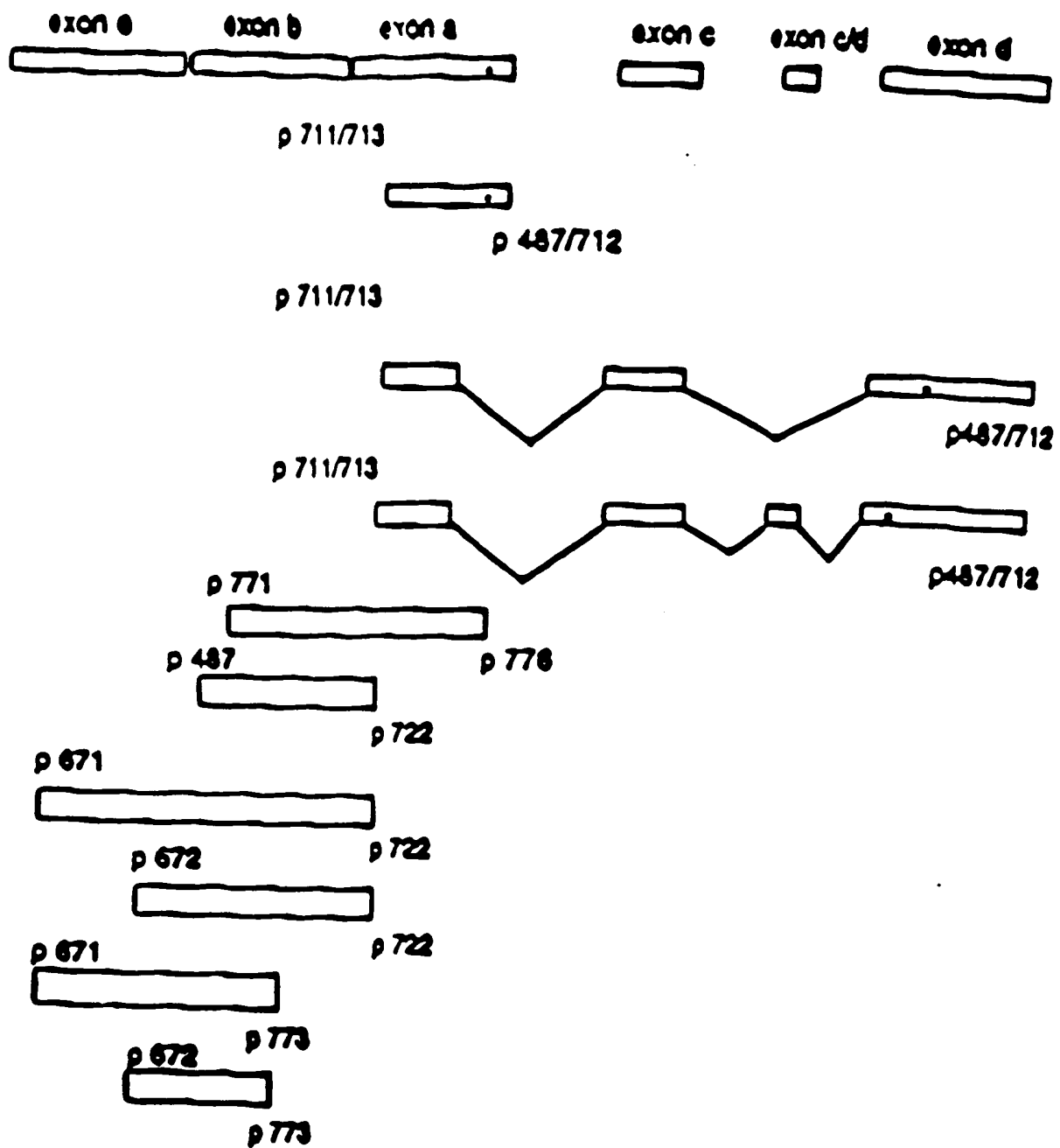


FIGURE 23

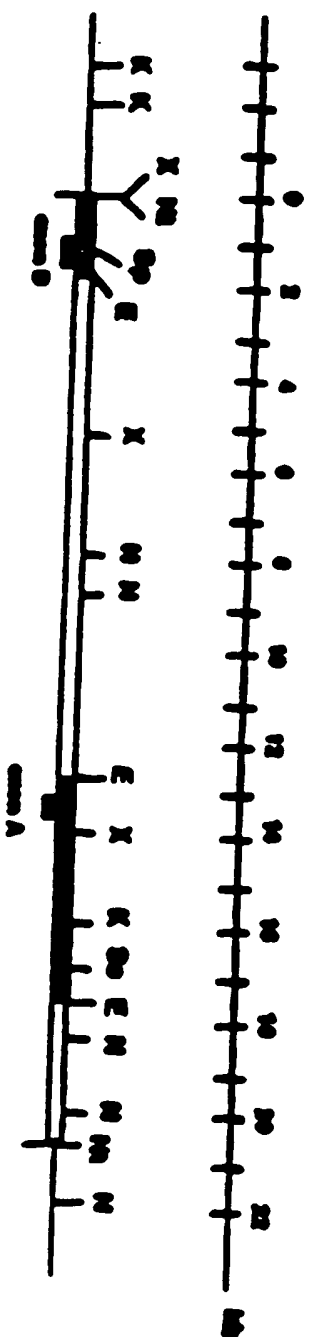


FIGURE 24

Alternative gene products of putative bovine GGF-9

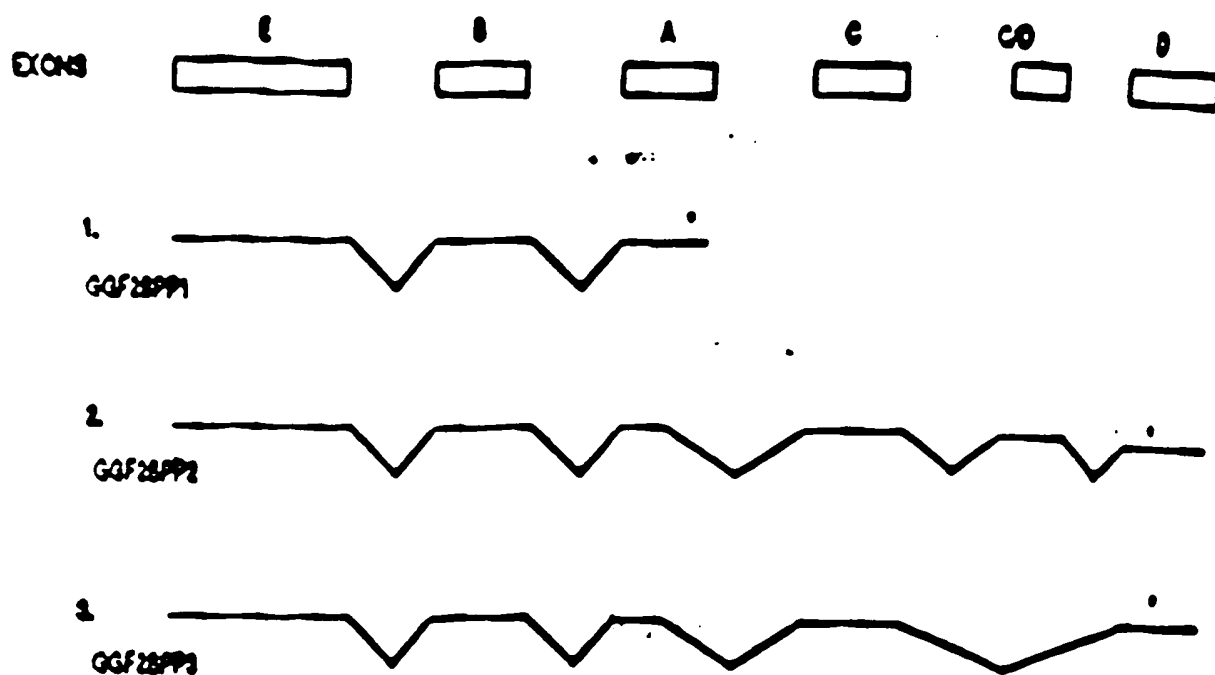


FIGURE 25

007-11 protein identified in deduced sequences of putative 007-11 proteins

| Peptide | Pos. | Sequence Match | |
|---------|------|--|--------------------------------------|
| II-1 | 1: | VHQVWAAR HQVWAAR AAGLR | (SEQ ID NO: 120) |
| II-10 | 14: | DLLLV GGLR dellev RLGAR | (SEQ ID NO: 121) |
| II-03 | 21: | LGAWGPPAFPVYR LLVR lgaughpa fpeay RLKED | (SEQ ID NO: 122) (SEQ ID NO: 123) |
| II-02 | 41: | YIFTHPELXSSG KEDSR YIFTHPELXSSG GPGRL | (SEQ ID NO: 124) (SEQ ID NO: 125) |
| II-6 | 103: | LVLK VAGSR LVLK CETSS | (SEQ ID NO: 126) |
| I-18 | 112: | EYKCLKFKWTFQATVH CETSS eysslkfkv fngsel SRDKE | (SEQ ID NO: 127) (SEQ ID NO: 128) |
| II-12 | 151: | KSLADSGEYHCK ELRIS KSLADSGEYHCK VTSKL | (SEQ ID NO: 129) (SEQ ID NO: 130) |
| I-07 | 152: | ASLADGEYHCK LRISK asladsgey hck VTSKL | (SEQ ID NO: 131) (SEQ ID NO: 132) |

FIGURE 26

(SEQ ID NO: 133)

FIGURE 27 1/3

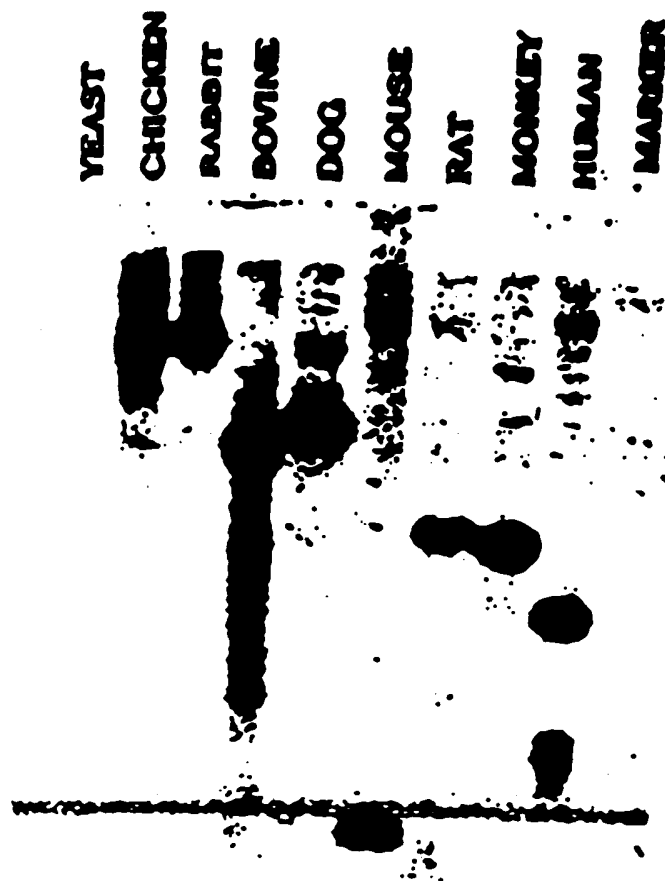


FIGURE 28

FIGURE 29

De novo GAG Gene Products

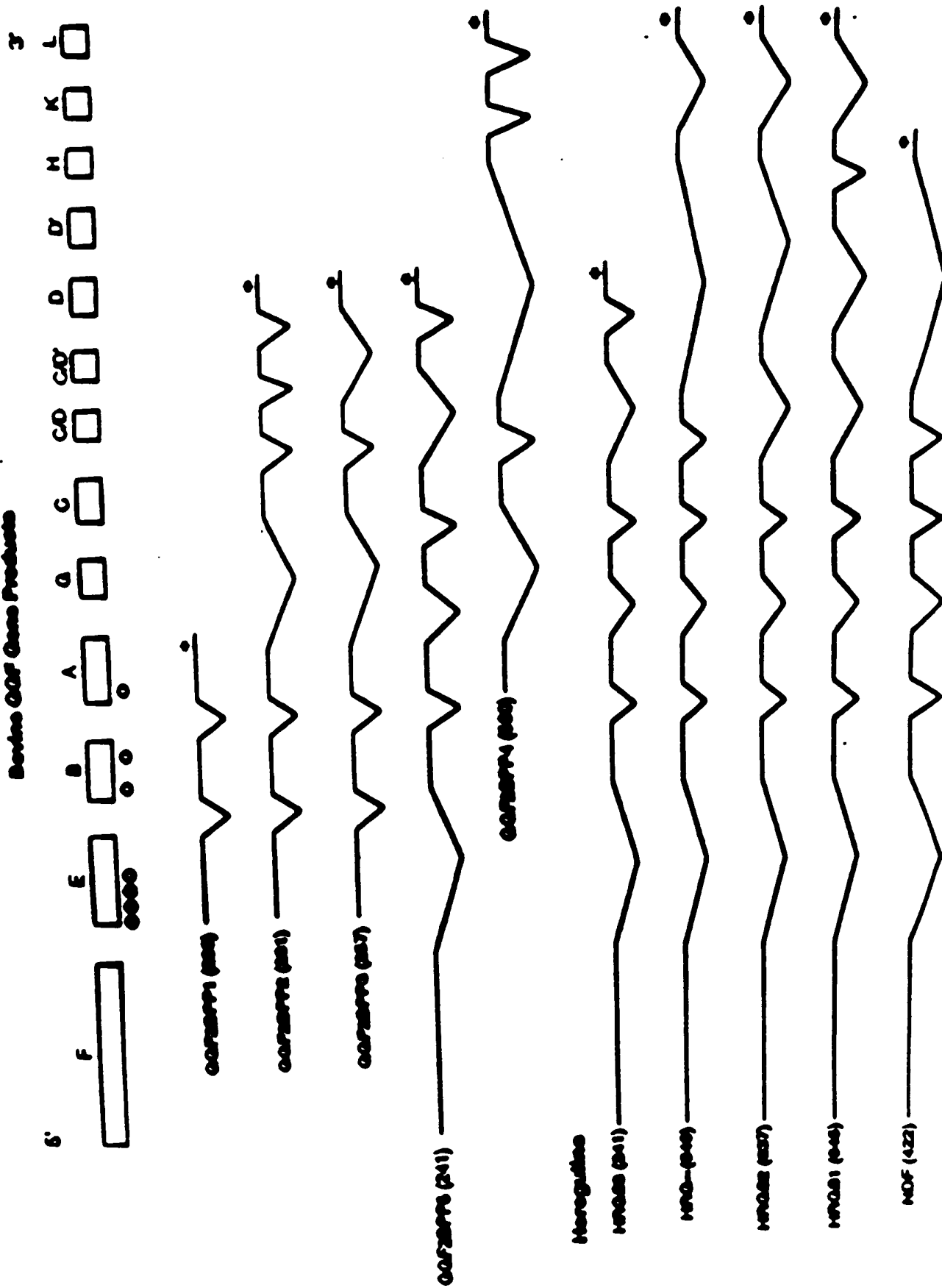


FIGURE 30

COOING SEGMENTS OF GLIAL GROWTH FACTOR/NEREGULIN GENE

COOLING SEGMENT P1. (SEQ ID NO: 136)

[illegible]

CODING SEGMENT 8: (SEQ ID NO: 137)

CCCATCAGTGTGCGCGCGGAAAGCCGCGCGCTTGAAGAAAGCACTGCGTCTCTACCGTGC 60
 N Q V W A A K A G G L K K D S L L T V R
 GCGTGGCGGCTCTGCGCCACCCCGCCTTCCCTCTCTGCGCGCGCTCAAGGAGGACAGCA 120
 L G A W G N P A P P S C G R L K E D S R
 GGTACATCTTCTTCAATGGAAGCCGAGGCCAACAGCAAGCGGCGCGCGCGCGCTCTCGCA 180
 Y I P P N E P E A N S S G G P G R L P S
 GCCTCGCTCTCCCCCTCTCGAGACGGGCGCGAACCTCAAGAAAGGAGGTCAGCCCGGTGCTG 240
 L L P P S R D G P E P Q E G G Q P G A V
 TCCAAAGCTGCTG : 32

CODING SEGMENT B: (SEQ ID NO: 138)

L P P R L K E N E S Q E S V A G S R L V
 CCTTCCCTCCCCCTTGAAGAGATGAAGAGTCAGGAGTCTGTGCCAGGTTCCAACTAG 60
 |||||
 ccttgcctccccgattgaaagagatgaaagccagggaatcggtgcagggtccaaactag
 Q A

L R C E T S S E Y S S L K P E V P E N G
 TCGTTCGGTCCGAGACCAGTTCTGAATACTCCTCTCTCAAGTTCAAGTGGTTCAAGATG 120
 |||||
 tccctcggtgtgaaaccagttctgaatactcctctctcagattcaagtgggtcaaggaatg
 R

S E L S R K N K P Q N I K I Q E R P G
 GGAGTGAATTAAGCCGAAAGAACAAACCAAAACATCAAGATACAGAAAGCCCGGG 170
 |||||
 ggaatgaattgaatcgaaaaaacaaaccacaaaatatcaagatacaaaaaagccagg
 N H K

CODING SEGMENT A: (SEQ ID NO: 139)

K S E L R I S K A S L A D S G E Y N C K
 GAAGTCAGAACTTCCGATTAGCAAGCGTCACTGCGCTGATTCTCGAGAAATATATGTGCAA 60
 |||||
 gaagtcaaggacttcgcattaaacaaagcatcactgggtgattctggagagtatatgtgcaa
 N

V I S K L G N D S A S A N I I V E S N
 AGTGATCAGCAAACTAGGAAATGACAGTGCCTCTGCCAACATCACCATTGTGCAAGTCAA 120
 |||||
 agtgatcagcaaaattaggaaatgacagtgcctctgccaaatatcaccatcgtggaatcaaa
 A
 CG 122
 ||
 CG

CODING SEGMENT A': (SEQ ID NO: 140)

TCTAAAACTACAGAGACTGTATTTTATGATCATCATAGTTCTGTGAATATACTTAAAC 60
 K S E L R I S K A S L A D
 CGCTTTGCTCCTGATCTTTGTAGCAAGTCAGAACTTCCGATTAGCAAGCGTCACTGCGCTG 120
 S G E Y N C K V I S K L G N D S A S A N
 ATTCTCGAGAAATATATGTGCAAGTATCAGCAAACTAGGAAATGACAGTGCCTCTGCCA 180
 I T I V E S N G K R C L L R A I S Q S L
 ACATCACCATTGTGCAAGTCAAGGTAAGAGATGCCTACTGCGTCTATTCTCAGTCTC 240
 R G . . . K . . . C . . .
 TAAAGGATTCATCAAGGATATGCTGCTACAGTTTCAATCAGGAGGTTGTTGAAATGTCAT 300

487

(SEQ ID NO: 141)

60

102

(SDQ ID NO: 160)

60

120

120

FIGURE 30 4/8

CODING SEGMENT C/D: (SEQ ID NO: 142)

K C Q P G F T G A R C T E N V P N E V Q
 AAGTGCCCAACCTGGATTCACTGGAGCGAGATGTACTGAGAATGTGCCCCATCAAAGTCCAA 60
 |||||
 aagtgcccaacctggattcactggagcgaagatgtactgagaatgtgccccatgaaagtccaa

T Q E
 ACCCAAGAA 69
 |||||
 acccaagaa
 N

CODING SEGMENT C/D': (SEQ ID NO: 143)

K C P N E F T G D R C Q N Y V N A S F Y
 AAGTGCCCAAAATGAGTTTACTGGTGATCGCTGCCAAAAGTACGTAATGGCCAGCTTCTAG 60
 |||||
 aagtgcccaaatgagtttactggatcgctgccaaaagtacgtaatggccagcttctag

CODING SEGMENT D: (SEQ ID NO: 144)

S T S T P F L S L P E Q
 AGTACGTCCCACTCCCTTTCTGTCTCTGCTGAATAG 36
 |||||
 agtacgtccactccctttctgtctctgctgaatag

CODING SEGMENT D': (SEQ ID NO: 145)

K E L G I E F N E
 aagcatcttgggattgaatttatggag 27

ACATAAGCTTATAGCTCAGCTAAGGAGAAACAGGCTCCACAGATCCAAAGCATGCCAG?
 N N L I A E L R R N R A N R S R C N Q I
 CCAgCTTTCGGCACTCATCTTAGAGCTTCTTCCATTCCCCATTGGGCTTCATTCTCTAA
 Q L S A T N L R A S S I P N W A S P S R
 GAGCCCTTGGCCTTCAgCAAG
 T P N P L G R

CODING SEGMENT L: (SEQ ID NO: 147)

[illegible]



480

940

600

660

720

TTAAATTAAICHA 733
|||||
EEAAAEAAACAA

GG728PP2 nucleotide sequence and deduced protein sequence

CATCATGTGTGGCGCGCGAAGCCGCGCGCTTGAAGAACTCGCTGCTCAACGTCG 10
 H Q V W A A K A G G L K K D S L L T V R
 CTGCGCGCGCTCGCGCCACCCCGCTTCTCTCTCTGCGCGCGCTCAAGGAGGACAGCAG 120
 L G A W G H P A P P S C G R L K E D S R
 TACATCTTCTTCAATGAGCGCCAGCGCCAAAGCAAGCGGCGCGCGCGCGCGCTTCCGAGC 180
 Y I P P H E P E A H S S G G P G R L P S
 CT 240
 L L P P S R D G P S P Q S G G Q P G A V
 CAACGCTGCGCGCTTCT 300
 Q R C A L P P R L K S H K S Q E S V A G
 TCCAACTAGTGTCT 360
 S K L V L R C E T S S E Y S S L K P K H
 CTCAGAAATCGGAGTGAATTAAAGCCGAAAGCAACCAAGAAAATCAAGATACAGAA 420
 P K H G S E L S R K H K P E H I K I Q K
 AGCGCGCGCGAAGTCAGAACTTCCATTAGCAAGCGTCACTCGCTGATTCTCGAGAAATAT 480
 R P G K S E L R I S K A S L A D S G E Y
 ATGTGCAAAAGTGATCAGCAAACTAGCAAAATGACAGTGGCTCTCTGCAACATCAACCATTTG 540
 N C K V I S K L G H D S A S A H I T I V
 GAGTCAAACCGCCACATCCACATCTACAGCTGGGACAAGCCATCTTGTCAAGTGTGACAG 600
 E S H A T S T S T A G T S H L V K C A E
 AAGGAGAAAICTTTCTGTGTGAATCGAGCGAGTCTTCAATGGTCAAGAGCTTTTCAAA 660
 K E K T P C V H G G E C P H V K D L S H
 CCTTCAAGATACTTGTGCAAGTGGCAACCTCGATTCACTCGAGCGAGATGTACTCAAGAT 720
 P S R Y L C K C Q P G P T G A R C T E H
 GTGCCCATCAAGTCCAAACCCCAAGAAAGTCCCAATCAAGTTTACTGGTCAATCGCTGC 780
 V P H E V Q T Q E K C P H E P T G D R C
 CAAACTACGTAATGGCCAGCTTCTACAGTACGTCCACTCCCTTTCTGTCTCTCTCTCTCT 840
 Q H Y V H A S P Y S T S T P P L S L P E
 TAGCGCATCTCAGTGGTCCCGCTTCTTGTGCGCGCATCTCCCTCAGATTCTCTCCAG 900
 .
 AGCTAGATGCGTTTTTACCAGGTCTAACATGACTGCGCTGTGCTGTGCGCATGAGAACATT 960
 AACACAAGCGATTGTATGACTTCTCTGTCTCGTACTAGTGGGCTCTGAGCTACTCTGAG 1020
 GTGCGTAAGGCTCCAGTGTTTCTCAATTGATCTCAATTACTGTGATCCACATGATAG 1080
 TCCCTCTCAACCGAGTCCAAATGACAAATAAAGCGCTTCAAAAGTCAAAAAAAAAAAAA 1140

FIG RE 31 2/2

TGA CTTCCTCTGTCCGTGA CTAGTGGCTCTGAGCTACTCGTAGGTCCGTAAAGGCTCCAG 1380
 TGT TTTCTGA AATTGATCTTGAATTACTGTGATACGACATGATAGTCCCTCTCAGCCAGT 1440
 CAATGACAAATAAAGGCTTGAAAAGTCTCACTTTTATTGAGAAAATAAAAATCGTTCCAG 1500
 GCGACAGTCCCTCTTCTTTATAAAATGACCCTATCCTTGAAAAGGAGGTGTGTTAAGTT 1560
 TAACCAGTACACACTTGAAATGATCGTAA GTTCGGTTCCGTTTCAGAA TGTGTTCTTTCTG 1620
 ACAAAATAAACAGAA TAAAAA AAAAAA 1683

CGP28994 nucleotide sequence and deduced protein sequence

GAAGTCAGAACTTCCATTAGCAAGCGTCACTCGGCTCAATTCGAGAAATATGTGCCA 60
 K S E L R I S K A S L A D S G S Y N C R
 AGTCATCAGCAAACTAGCAATGACAGTGGCTCTGCCAACATCACCATTGTGAGTCAAA 120
 V I S K L G N D S A S A N I T I V E S N
 CGCCACATCCACATCTACAGCTGGGACAAAGCCATCTTGTCAAGTGTGCAGAGAGAGAA 180
 A T S T S T A G T S E L V K C A E K E R
 AACTTTCTGTGTGAATGGAGCGGACTGCTTCATGGTGAAGAAGCTTTCAATCCCTCAAG 240
 T P C V N G G D C F N V K D L S N P S R
 ATACTTGTCAAGTCCCAACCTGGATTCACTCGAGCCAGATGTACTCAGAAATGTGCCCA 300
 Y L C K C Q P G F T G A R C T E N V P N
 GAAAGTCCAAACCCAAAGAAAAGCCGAGGAGCTGTACCAAGAGAGTGTCTCACCATTAC 360
 K V Q T Q E K A E E L Y Q K R V L T I T
 CGGCATTTCATCGCGCTGCTGTGGTTGGCATCATGTGTGTGTGTGTCTACTGCCAAAC 420
 G I C I A L L V V G I N C V V V Y C K T
 CAAGAAACAAACCGAAAAAGCTTCATGACCGGCTTCGGCAGAGCTTCGGTCTGAAGAAA 480
 K K Q R K K L E D R L R Q S L R S E R N
 CACCATCATGAACGTAGCCAAAGGCCCCAACCACCCCAATCCGCCCCCGAGAACGTGCA 540
 T N N N V A N G P E E P N P P P E N V Q
 GCTGGTGAATCAATACGTATCTAAAAATGTTCATCTCTAGCGAGCATATTGTTCAGAGAG 600
 L V N Q Y V S K N V I S S E E I V E R E
 GCGCGAGAGCTCTTTTCCACCAGTCACTACACTTCGACAGCTCATCATTCCTACTGT 660
 A E S S F S T S E Y T S T A E E S T T V
 CACTCAGACTCCCAGTCAAGCTGGAGCAATGGACACACTGAAGCATCATTCGGAAG 720
 T Q T P S E S W S N G E T E S I I S E S
 CCACTCTGTCAATCGTGAATGTCAATCGTAGAAAACAGTAGGCACAGCAAGCCCACTGGGG 780
 H S V I V N S S V E N S R E S S P T G G
 CCGCAGAGGAGCTCTCAATGGCTTGGGAGGCGCTCTGTAATGTAAAGCTTCTCAGGCA 840
 P R G R L N G L G G P R E C H S F L R E
 TCCAGAGAAACCCCTGACTCTTACCGAGACTCTCTCTCATAGTCGAAGACATAACCTTAT 900
 A R E T P D S Y R D S P E S E R E N L I
 AGCTGAGCTAAGGAGAAACAAAGGCCACAGATCCAAATGATGCAGATCCAGCTTTCCGC 960
 A E L R R N K A E R S K C N Q I Q L S A
 AACTCATCTTAGAGCTTCTTCCATTCCCCATTGGGCTTCATTCTCTAAGACCCCTTGGCC 1020
 T H L R A S S I P N W A S F S K T P W P
 TTEAGGAAGGTATGTATCAGCAATGACCACCCCGGCTCGTATGTACCTGTAGATTTCCA 1080
 L G R Y V S A H T T P A R N S P V D F H
 CAGCCCAAGCTCCGCAAGTCAAGCCCTTCGGAATGTCTCTGCGCTGTCTCAGCACGAC 1140
 T P S S F Y S P P S E M S P P Y S S T T

FIGURE 33 2/2

GGTCTCCATGCCCTCCATGCGCGTCACTCCCTTCGTCGAAGAGGAGAGACCCCTGCTCT 1200
 V S N P S N A V S P P V E E E R P L L L
 TGTACGCCACCACTGGCTGCGGAGAACTATGACCAACAAGCCCAAGCAATTCAACTGTT 1260
 V T P P R L R E K Y D N N A Q Q P N S P
 CCACTGCAACCCCTGCGCATGAGAGCAACAGCTGCCCCCAGCCCCCTGACGATAGTGA 1320
 N C N P A N E S N S L P P S P L R I V E
 GGATACGGAATATGAAACGACCCAGGAGTACGAACCAAGTCAAGAGCCCGTTAAGAACT 1380
 D E E Y E T T Q E Y E P A Q E P V K E L
 CACCAACAGCAGCCCGCGGCGCAAAAGAACCAAGCCCAATGGTCAATTCGCCACAGTT 1440
 T N S S R R A K E T K P N G N I A E R L
 GGAATGGAACAACAACAGCGCGTACAGCAGTAACTCAGAGAGCGAAACAGAGCATGA 1500
 E N D N N T G A D S S N S E S E T E D E
 AAGAGTAGGAGAAGATACGCCTTCCTGCGCATAACAGAAACCCCTGCGACCCAGTCTGA 1560
 R V G E D T P P L A I Q N P L A A S L E
 GCGCGCCCTGCGCTTCGCGCTGGTGCACAGCAGGACTAAACCAACAGCGCGCTTCTCTCC 1620
 A A P A P R L V D S R T N P T G G P S P
 GCAGGAAGAATTGCAGGCCAGGCTCTCCGTGTAAATCGCTAACCAAGACCCCTATCGCTGT 1680
 Q E E L Q A R L S G V I A N Q D P I A V
 CTAAACCGAAATACACCCATAGATTCACTGTAAAACTTTATTTTATATAATAAAGTAT 1740
 TCCACCTTAATTAAACAAAA 1764

FIGURE 34

.
GGF2Doo5KCAEKEKTFVNGGECFMYKDLSNPSRYLCKCPNEFTGDRCONYVMASFY 1
GGF2Doo4KCAEKEKTFVNGGDCFMYKDLSNPSRYLCKCQPGFTGARCTENVPMKVQ 2
DEGE ECLRKYKDFCIH - GECKYVKELRAPS — CKCQOEYFGERCGEKSARKHS 3

1(SDQ ID NO: 151)

2(SDQ ID NO: 152)

3(SDQ ID NO: 153)

FIGURE 35

**200 kDa tyrosine phosphorylation
compared with mitogenic activity**

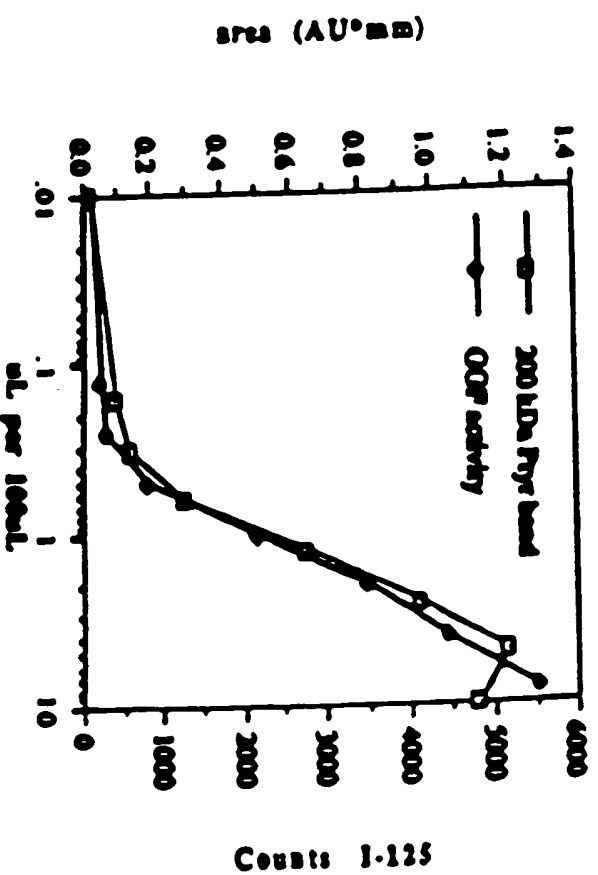


FIGURE 36 172

GGT/REGULON SPLICING VARIANTS

F-B-A'

F-B-A-C-C/D-D
F-B-A-C-C/D-E
F-B-A-C-C/D-E-L
F-B-A-C-C/D-E-K-L
F-B-A-C-C/D-D'-E
F-B-A-C-C/D-D'-E-L
F-B-A-C-C/D-D'-E-K-L
F-B-A-C-C/D'-D
F-B-A-C-C/D'-E
F-B-A-C-C/D'-E-L
F-B-A-C-C/D'-E-K-L
F-B-A-C-C/D'-D'-E
F-B-A-C-C/D'-D'-E-L
F-B-A-C-C/D'-D'-E-K-L
F-B-A-C-C/D'-D'-E-K-L
F-B-A-C-C/D-C/D'-D
F-B-A-C-C/D-C/D'-E
F-B-A-C-C/D-C/D'-E-L
F-B-A-C-C/D-C/D'-E-K-L
F-B-A-C-C/D-C/D'-D'-E
F-B-A-C-C/D-C/D'-D'-E-L
F-B-A-C-C/D-C/D'-D'-E-K-L

F-E-B-A'

F-E-B-A-C-C/D-D
F-E-B-A-C-C/D-E
F-E-B-A-C-C/D-E-L
F-E-B-A-C-C/D-E-K-L
F-E-B-A-C-C/D-D'-E
F-E-B-A-C-C/D-D'-E-L
F-E-B-A-C-C/D-D'-E-K-L
F-E-B-A-C-C/D'-D
F-E-B-A-C-C/D'-E
F-E-B-A-C-C/D'-E-L
F-E-B-A-C-C/D'-E-K-L
F-E-B-A-C-C/D'-D'-E
F-E-B-A-C-C/D'-D'-E-L
F-E-B-A-C-C/D'-D'-E-K-L
F-E-B-A-C-C/D-C/D'-D
F-E-B-A-C-C/D-C/D'-E
F-E-B-A-C-C/D-C/D'-E-L
F-E-B-A-C-C/D-C/D'-E-K-L
F-E-B-A-C-C/D-C/D'-D'-E
F-E-B-A-C-C/D-C/D'-D'-E-L
F-E-B-A-C-C/D-C/D'-D'-E-K-L

F-B-A-G-C-C/D-D
F-B-A-G-C-C/D-E
F-B-A-G-C-C/D-E-L
F-B-A-G-C-C/D-E-K-L
F-B-A-G-C-C/D-D'-E
F-B-A-G-C-C/D-D'-E-L
F-B-A-G-C-C/D-D'-E-K-L
F-B-A-G-C-C/D'-D
F-B-A-G-C-C/D'-E
F-B-A-G-C-C/D'-E-L
F-B-A-G-C-C/D'-E-K-L
F-B-A-G-C-C/D'-D'-E
F-B-A-G-C-C/D'-D'-E-L
F-B-A-G-C-C/D'-D'-E-K-L
F-B-A-G-C-C/D-C/D'-D
F-B-A-G-C-C/D-C/D'-E
F-B-A-G-C-C/D-C/D'-E-L
F-B-A-G-C-C/D-C/D'-E-K-L
F-B-A-G-C-C/D-C/D'-D'-E
F-B-A-G-C-C/D-C/D'-D'-E-L
F-B-A-G-C-C/D-C/D'-D'-E-K-L

F-E-B-A-G-C-C/D-D
F-E-B-A-G-C-C/D-E
F-E-B-A-G-C-C/D-E-L
F-E-B-A-G-C-C/D-E-K-L
F-E-B-A-G-C-C/D-D'-E
F-E-B-A-G-C-C/D-D'-E-L
F-E-B-A-G-C-C/D-D'-E-K-L
F-E-B-A-G-C-C/D'-D
F-E-B-A-G-C-C/D'-E
F-E-B-A-G-C-C/D'-E-L
F-E-B-A-G-C-C/D'-E-K-L
F-E-B-A-G-C-C/D'-D'-E
F-E-B-A-G-C-C/D'-D'-E-L
F-E-B-A-G-C-C/D'-D'-E-K-L
F-E-B-A-G-C-C/D-C/D'-D
F-E-B-A-G-C-C/D-C/D'-E
F-E-B-A-G-C-C/D-C/D'-E-L
F-E-B-A-G-C-C/D-C/D'-E-K-L
F-E-B-A-G-C-C/D-C/D'-D'-E
F-E-B-A-G-C-C/D-C/D'-D'-E-L
F-E-B-A-G-C-C/D-C/D'-D'-E-K-L

FIGURE 36

007/REDBOULIN IMPLICIT VARIANTS CONTINUED

E-B-A'

E-B-A-C-C/D-D
E-B-A-C-C/D-E
E-B-A-C-C/D-E-L
E-B-A-C-C/D-E-K-L
E-B-A-C-C/D-D'-E
E-B-A-C-C/D-D'-E-L
E-B-A-C-C/D-D'-K-K-L
E-B-A-C-C/D'-D
E-B-A-C-C/D'-E
E-B-A-C-C/D'-E-L
E-B-A-C-C/D'-E-K-L
E-B-A-C-C/D'-D'-E
E-B-A-C-C/D'-D'-E-L
E-B-A-C-C/D'-D'-E-K-L
E-B-A-C-C/D-C/D'-D
E-B-A-C-C/D-C/D'-E
E-B-A-C-C/D-C/D'-E-L
E-B-A-C-C/D-C/D'-E-K-L
E-B-A-C-C/D-C/D'-D'-E
E-B-A-C-C/D-C/D'-D'-E-L
E-B-A-C-C/D-C/D'-D'-E-K-L

E-B-A-C-C-C/D-D
E-B-A-C-C-C/D-E
E-B-A-C-C-C/D-E-L
E-B-A-C-C-C/D-E-K-L
E-B-A-C-C-C/D-D'-E
E-B-A-C-C-C/D-D'-E-L
E-B-A-C-C-C/D-D'-E-K-L
E-B-A-C-C-C/D'-D
E-B-A-C-C-C/D'-E
E-B-A-C-C-C/D'-E-L
E-B-A-C-C-C/D'-E-K-L
E-B-A-C-C-C/D'-D'-E
E-B-A-C-C-C/D'-D'-E-L
E-B-A-C-C-C/D'-D'-E-K-L
E-B-A-C-C-C/D-C/D'-D
E-B-A-C-C-C/D-C/D'-E
E-B-A-C-C-C/D-C/D'-E-L
E-B-A-C-C-C/D-C/D'-E-K-L
E-B-A-C-C-C/D-C/D'-D'-E
E-B-A-C-C-C/D-C/D'-D'-E-L
E-B-A-C-C-C/D-C/D'-D'-E-K-L

AGCCATCTTGTCAAGTGTGCAGAGAACGAGAAAACCTTTCTGTGTGAATGGAGCGGAGTGC
S H L V R C A E K E K T P C V N G G E C
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTGGCCAAATGAGTTT
P N V K D L S N P S R Y L C K C P N E P
ACTGGTGATCGCTGCCAAAAGTACGTAATGGCCAGCTTCTACAGTACGTCCACTCCCTTT
T G D R C Q N Y V N A S P Y S T S T P P
CTGTCTCTGCCTGAATAG
L S L P E •

(SEQ ID NO: 154)

FIGURE 37

AGCCATCTTGTCAAGTGTGCAGAGAACGAGAAAACCTTCTGTGTGAATGGACCCGAGTGC
S N L V K C A E E E K T F C V N G G E C
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTCCCAACCTGGATTG
F N V K D L S N P S R Y L C K C Q P G P
ACTCGAGCCAGATGTACTGAGAAATGTGCCCATGAAAGTCCAAACCCAAAGAAAAGCCGAG
T G A R C T E N V P N K V Q T Q E K A E
GAGCTCTACTAA
E L Y •

(SEQ ID NO: 155)

FIGURE 38

ACCCATCTTGTCAAGTGTGCAGAGAGGAGAAAAGTTTCTGTGTGAATGGAGGGGAGTGC
 S H L V K C A E K E K T P C V N G G E C
 TTCATCGTGAAAGACCTTTCAATCCCTCAAGATACTTGTGCAAGTGGCCAAATGAGTTT
 P H V K D L S N P S R Y L C K C P H E P
 ACTCGTGATCGGTGCCAAAAGTACCTAATGGCCAGCTTCTACAAAGCGGAGGAGCTCTAC
 T G D R C Q N Y V H A S P Y K A E E L Y
 TAA
 .

(SEQ ID NO: 156)

FIGURE 39

IGFLA

AGCCATCTTGTCAAGTGTGCAGAGAGGACAAAACCTTTCTGTGTGAATGGAGCGGAGTGC
S H L V K C A E E E K T P C V N G G E C
TTCATCGTGAAAGACCTTTCAAATCCCTCAAGATACTTGTCGAAGTGCCCAAATGAGTTT
P H V K D L S N P S R Y L C K C P N E P
ACTGGTGATCGCTGCCAAAACCTACCTAATCGCCAGCTTCTACAAGCATCTTGGGATTCAA
T G D R C Q N Y V N A S P Y K E L G I E
TTTATCGAGAAAGCGGAGGAGCTCTACTAA
P H E K A E E L Y •

(SEQ ID NO: 157)

FIGURE 40

EGFLS

AGCCATCTTGTCAAGTGTGCAGACAAGGAGAAAACCTTCTGTGTGAATGGAGGCGAGTGC
S N L V K C A E K E K T P C V N G G E C
TTCATGGTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTGCCAAGCTGGATTG
P N V K D L S N P S R Y L C K C Q P G P
ACTGGAGCGAGATGTACTGAGAATGTGCCCATGAAAGTCCAAACCCAAAGAAAAGTGCCCA
T G A R C T E N V P N K V Q T Q E K C P
AATGAGTTTACTGGTGATCGCTGCCAAAACCTACGTAATGGCCAGCTTCTACAGTACGTC
N E P T G D R C Q N Y V N A S P Y S T S
ACTCCCTTTCTGTCTCTGCCTCAATAG
T P P L S L P E .

(SEQ ID NO: 158)

FIGURE 41

AGCCATCTTGTCAAGTGTGCAGAGACGAGAAAAGTTTCTGTGTGAATCGAGGCGAGTCC
 S N L V K C A E K E K T P C V H G G E C
 TTCATGGTGAAAGACCTTTCAATCCCTCAAGATACTTGTGCAAGTGCCAACTCGGATTG
 P H V K D L S N P S R Y L C K C Q P G P
 ACTCGAGCGAGATGTACTGAGAAATGTGCCCATGAAGTCCAAACCCAGAAAAGTGCCCA
 T G A R C T E N V P H K V Q T Q E K C P
 AATGAGTTTACTGGTGATCGCTGCCAAAAGTACGTAATGCCAGCTTCTACAAAGCGGAG
 N E P T G D R C Q H Y V H A S P Y K A E
 GAGCTCTACTAA
 E L Y •

(SEQ ID NO: 159)

FIGURE 42

GGF2HBS5

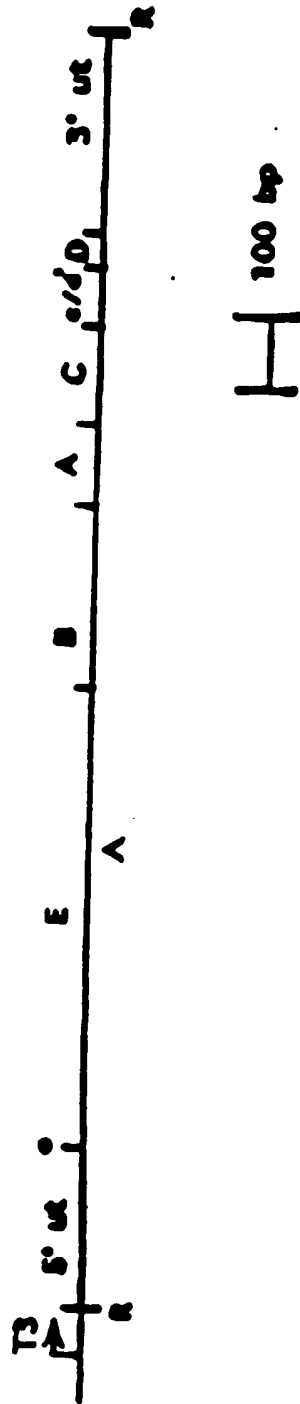


FIGURE 43

| | | | | | | |
|--|-------------------------|---------------|----------------|--------------|-----|---|
| GGAAATGCTTTT | TTTTTTTTTTTCTC | CAATTTTTTTTTT | CGGCTAAAGCTT | CGGC | 60 | • |
| TTTCTGTGAT | TCCATCCACTTCT | TTCGCGCTCTCT | CTCCATTAACAACT | CTCTCGCGCT | 120 | • |
| CCACCGCCAT | GAATGAATGA | AAACAGCAAGCC | CAAGCGCGCGCG | CGCGCGCGCGCG | 180 | • |
| CGAAGCGCA | AGCAAGCAAGCC | CAAGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | 240 | • |
| AGCAAGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | 300 | • |
| <div style="text-align: center;">N E W E E A P E E S G E</div> | | | | | | • |
| CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | 360 | • |
| P G P E A G E P | G S A A E S S P | P P L P L | | | | • |
| CTCCACTA | CTCTCTCTCT | CTCTCTCTCTCT | CTCTCTCTCTCT | CTCTCTCTCTCT | 420 | • |
| L P L L L L G T | A A L A P G A A G H | | | | | • |
| <div style="text-align: center;">V C L L T V A A L P P T</div> | | | | | | • |
| <div style="text-align: center;">GGFII-9</div> | | | | | | • |
| CAAGCGCGCT | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | 480 | • |
| E A A P A G A S | V C T S S P P S V G S V | | | | | • |
| <div style="text-align: center;">A S P V S V G S V</div> | | | | | | • |
| <div style="text-align: center;">GGFII-8</div> | | | | | | • |
| CAAGCGCTA | CTCAAGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | 540 | • |
| G E L A G E A A V | V I E G E V E P G E E | | | | | • |
| G E L V G E I W | F V V I E G E | | | | | • |
| <div style="text-align: center;">GGFII-4</div> | | | | | | • |
| CAAGCGCGCG | CTCAAGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | 600 | • |
| G G G A L D E E A | A A A A G E A G A W G | | | | | • |
| CGCGCTCGCG | CAAGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | 660 | • |
| G D E E P P A A G | P E A L G P P A E E P | | | | | • |
| CTCTCTCTCT | CAAGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | CGCGCGCGCGCG | 720 | • |
| L L A A H G T V | P S H P T A P V P S A G | | | | | • |

FIGURE 44 *i/3*

780
 E P Q E E A P Y L V E V E Q V W A V E A
 E V E Q V W A A E
 GCFII-1 & GCFII-11

840
 G G L E E D S L L T V R L Q T W Q E P A
 D L L L E V L Q A W Q P P A
 GCFII-10 GCFII-3

900
 P P S C G R L E E D S R Y I P F N E P D
 P P V E Y Y I P P N E P E
 GCFII-2

960
 A N S T S R A P A A P R A S P P P L E T
 A E S S G

1020
 G R N L E E E V S R V L C E R C A L P P

1080
 Q L E E M E S Q E S A A G S E L V L E C
 L V L E
 GCFII-6

1140
 E T S S E Y S S L E P E W P E N Q E E L

1200
 H E E H E P Q M I E I Q E E P Q E S E L

1260
 R I N K A S L A D S G E Y N C E V I S E
 K A S L A D S G E Y M E E
 GCFII-12

1320
 L G N D S A S A N I T I V E S H A T S T

FIGURE 44 2/3

| | | |
|--|------|---|
| TCCACCTGCGACACACCTTCTGAAAATGTCGCGACACACACCTTCTGCTG S T T G T S E L V E C A S E E E T P C V | 1380 | • |
| AACGACGCGCTGCTTCACTGTAAGACCTTCAACGCGCTGCGCTGCTGCTG H G G S C P N V E D L S N P S E T L C E | 1440 | • |
| TCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG C P N E P T G D E C Q N Y V N A S P Y S | 1500 | • |
| AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG T S T P P L S L P E | 1560 | • |
| TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1620 | • |
| TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1680 | • |
| TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1740 | • |
| TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1800 | • |
| AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1860 | • |
| AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1920 | • |
| AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1980 | • |
| AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 2040 | • |

FIGURE 44 3/3

FIGURE 45A

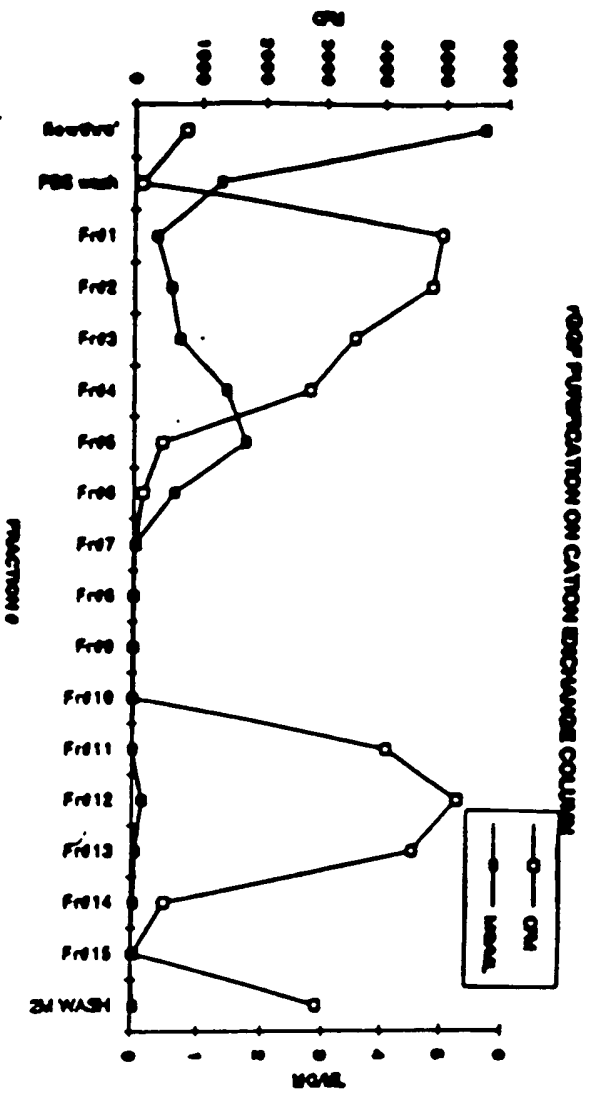
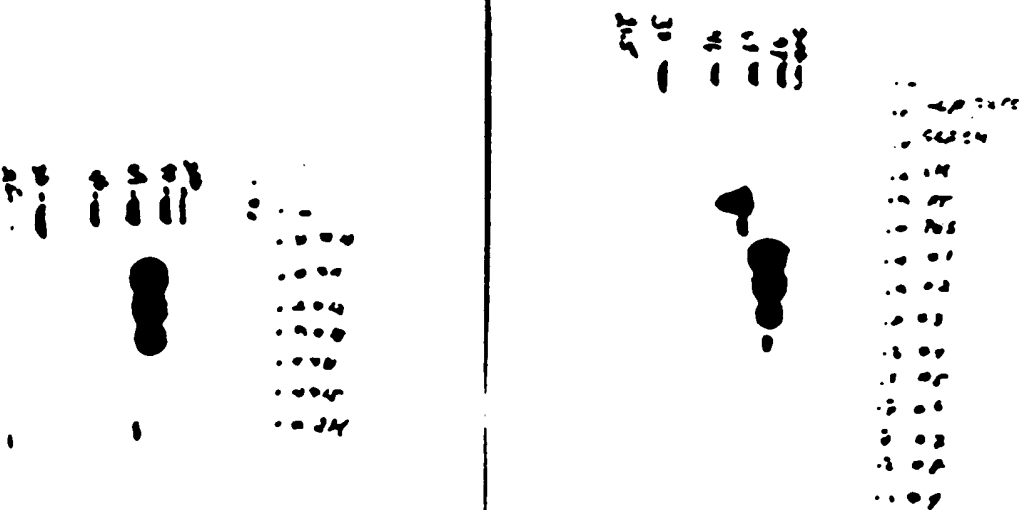


FIGURE 45B



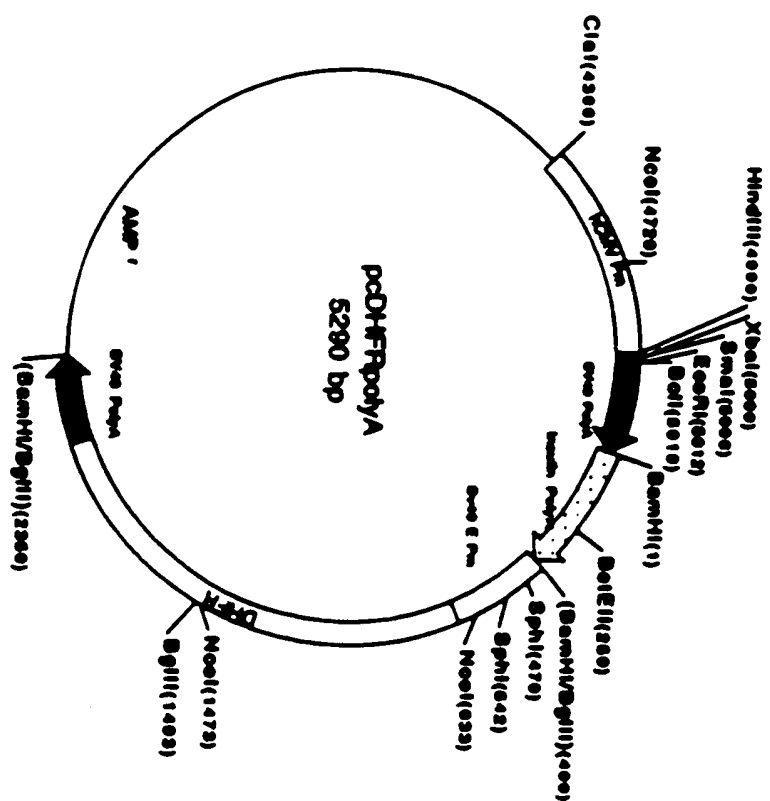


FIGURE 47